CRF Errors Corrected by the STIC Systems Branch

Serial Number: *10/046,643*   ENTERED

CRF Processing Date: 2/6/2002
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95
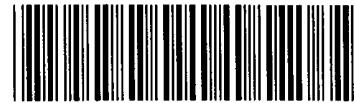
OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/046,643

DATE: 02/06/2002
TIME: 08:05:04

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02062002\J046643.raw

```
      4 <110> APPLICANT: Meyers, Rachel E.
      5       Millennium Pharmaceuticals Inc
      7 <120> TITLE OF INVENTION: 33449, A Human Protease Family Member
      8       and Uses Therefor
     10 <130> FILE REFERENCE: MPI2001-016P1RCP1(M)
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/046,643
C--> 12 <141> CURRENT FILING DATE: 2002-01-14
     12 <150> PRIOR APPLICATION NUMBER: 60/262,513
     13 <151> PRIOR FILING DATE: 2001-01-18
     15 <160> NUMBER OF SEQ ID NOS: 10
     17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 721
     21 <212> TYPE: DNA
     22 <213> ORGANISM: homo sapiens
     24 <220> FEATURE:
     25 <221> NAME/KEY: CDS
     26 <222> LOCATION: (115)...(615)
     28 <400> SEQUENCE: 1
     29 ccacgcgtcc gcttcggcgg ggcccaggtg agaaaggccc acctgtgtcc tggttgaggg 60
     30 tctccagggt tctttggggc tcgaggccaa tggtggcaga gtctacatag aact atg    117
     31                                                              Met
     32                                                                1
     34 ctt cgt ggt gtt ctg ggg aaa acc ttt cga ctt gtt ggc tat act att 165
     35 Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr Ile
     36               5                  10                  15
     38 caa tat ggc tgt ata gct cat tgt gct ttt gaa tac gtt ggt ggt gtt 213
     39 Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly Val
     40               20                  25                  30
     42 gtc atg tgt tct gga cca tca atg gag cct aca att caa aat tca gat 261
     43 Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser Asp
     44         35                  40                  45
     46 att gtc ttt gca gaa aat ctt agt cga cat ttt tat ggt atc caa aga 309
     47 Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln Arg
     48 50                  55                  60                  65
     50 ggt gac att gtg att gca aaa agc cca agt gat cca aaa tca aat att 357
     51 Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn Ile
     52                  70                  75                  80
     54 tgt aaa aga gta att ggt ttg gaa gga gac aaa atc ctc acc act agt 405
     55 Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr Ser
     56                  85                  90                  95
     58 cca tca gat ttc ttt aaa agc cat agt tat gtg cca atg ggt cat gtt 453
     59 Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His Val
```

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02062002\J046643.raw

```
60          100                   105               110
62 tgg tta gaa ggt gac aat cta cag aat tct aca gat tcc agg tgc tat    501
63 Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys Tyr
64     115                   120               125
66 gga cct att cca tat gga cta ata aga gga cga atc ttc ttt aag att    549
67 Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys Ile
68 130                   135               140               145
70 tgg cct ctg agt gat ttt gga ttt tta cgt gcc agc cct aat ggc cac    597
71 Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly His
72             150                   155               160
74 aga ttt tct gat gat tag taagcattta ttcttttgac ttgattattg          645
75 Arg Phe Ser Asp Asp  *
76             165
78 tctccttttc atgtgaattt attactcccg ttgaaaccgt gtacttacca ataaactatt 705
79 tgctattcaa aaaaaa                                                  721
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 166
83 <212> TYPE: PRT
84 <213> ORGANISM: homo sapiens
86 <400> SEQUENCE: 2
87 Met Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr
88  1               5                   10                  15
89 Ile Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly
90         20                  25                  30
91 Val Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser
92         35                  40                  45
93 Asp Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln
94     50                  55                  60
95 Arg Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn
96 65                  70                  75                  80
97 Ile Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr
98                 85                  90                  95
99 Ser Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His
100                 100                 105                 110
101 Val Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys
102         115                 120                 125
103 Tyr Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys
104     130                 135                 140
105 Ile Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly
106 145                 150                 155                 160
107 His Arg Phe Ser Asp Asp
108                 165
111 <210> SEQ ID NO: 3
112 <211> LENGTH: 501
113 <212> TYPE: DNA
114 <213> ORGANISM: homo sapiens
116 <220> FEATURE:
117 <221> NAME/KEY: CDS
118 <222> LOCATION: (1)...(501)
```

```
120 <400> SEQUENCE: 3
121 atg ctt cgt ggt gtt ctg ggg aaa acc ttt cga ctt gtt ggc tat act   48
122 Met Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr
123   1               5                  10                  15
125 att caa tat ggc tgt ata gct cat tgt gct ttt gaa tac gtt ggt ggt   96
126 Ile Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly
127             20                  25                  30
129 gtt gtc atg tgt tct gga cca tca atg gag cct aca att caa aat tca  144
130 Val Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser
131         35                  40                  45
133 gat att gtc ttt gca gaa aat ctt agt cga cat ttt tat ggt atc caa  192
134 Asp Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln
135      50                  55                  60
137 aga ggt gac att gtg att gca aaa agc cca agt gat cca aaa tca aat  240
138 Arg Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn
139  65                  70                  75                  80
141 att tgt aaa aga gta att ggt ttg gaa gga gac aaa atc ctc acc act  288
142 Ile Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr
143              85                  90                  95
145 agt cca tca gat ttc ttt aaa agc cat agt tat gtg cca atg ggt cat  336
146 Ser Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His
147             100                 105                 110
149 gtt tgg tta gaa ggt gac aat cta cag aat tct aca gat tcc agg tgc  384
150 Val Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys
151         115                 120                 125
153 tat gga cct att cca tat gga cta ata aga gga cga atc ttc ttt aag  432
154 Tyr Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys
155      130                 135                 140
157 att tgg cct ctg agt gat ttt gga ttt tta cgt gcc agc cct aat ggc  480
158 Ile Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly
159 145                 150                 155                 160
161 cac aga ttt tct gat gat tag                                       501
162 His Arg Phe Ser Asp Asp  *
163                  165
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 74
168 <212> TYPE: PRT
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: consensus
174 <400> SEQUENCE: 4
175 Gly Gly Ser Met Glu Pro Thr Leu His Asp Thr Gly Asp Arg Leu Phe
176   1               5                  10                  15
177 Val Asn Lys Phe Leu Tyr Gly Ile Lys Leu Pro Val Ile Asp Lys Thr
178             20                  25                  30
179 Val Lys Asn Thr Gly Gly Ile Lys Arg Gly Asp Ile Val Val Phe Lys
180         35                  40                  45
181 Ala Pro Thr Lys Pro Asn Val His Tyr Val Lys Arg Val Ile Gly Leu
182      50                  55                  60
```

●   ●

183 Pro Gly Asp Thr Val Lys Met Lys Asn Asp
184 65   70
187 <210> SEQ ID NO: 5
188 <211> LENGTH: 24
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: consensus
195 <400> SEQUENCE: 5
196 Gly Asp Asn Arg Leu Asn Ser Met Asp Ser Arg Tyr Gly Leu Gly Leu
197 1   5   10   15
198 Val Ala Leu Lys Asn Ile Val Gly
199   20
202 <210> SEQ ID NO: 6
203 <211> LENGTH: 189
204 <212> TYPE: PRT
205 <213> ORGANISM: Saccharomyces cerevisiae
207 <400> SEQUENCE: 6
208 Thr Val Gly Thr Leu Pro Ile Trp Ser Lys Thr Phe Ser Tyr Ala Ile
209 1   5   10   15
210 Arg Ser Leu Cys Phe Leu His Ile Ile His Met Tyr Ala Tyr Glu Phe
211   20   25   30
212 Thr Glu Thr Arg Gly Glu Ser Met Leu Pro Thr Leu Ser Ala Thr Asn
213   35   40   45
214 Asp Tyr Val His Val Leu Lys Asn Phe Gln Asn Gly Arg Gly Ile Lys
215   50   55   60
216 Met Gly Asp Cys Ile Val Ala Leu Lys Pro Thr Asp Pro Asn His Arg
217 65   70   75   80
218 Ile Cys Lys Arg Val Thr Gly Met Pro Gly Asp Leu Val Leu Val Asp
219   85   90   95
220 Pro Ser Thr Ile Val Asn Tyr Val Gly Asp Val Leu Val Asp Glu Glu
221   100   105   110
222 Arg Phe Gly Thr Tyr Ile Lys Val Pro Glu Gly His Val Trp Val Thr
223   115   120   125
224 Gly Asp Asn Leu Ser His Ser Leu Asp Ser Arg Thr Tyr Asn Ala Leu
225   130   135   140
226 Pro Met Gly Leu Ile Met Gly Lys Ile Val Ala Ala Asn Asn Phe Asp
227 145   150   155   160
228 Lys Pro Phe Trp Asp Gly Ser Ile Arg Asn Ile Trp Gly Phe Lys Trp
229   165   170   175
230 Ile Asn Asn Thr Phe Leu Asp Val Gln Ala Lys Ser Asn
231   180   185
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 5
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: consensus
242 <400> SEQUENCE: 7

```
243 Arg Arg Gly Asp Leu
244  1              5
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 14
249 <212> TYPE: PRT
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: consensus
255 <221> NAME/KEY: VARIANT
256 <222> LOCATION: 1,2
257 <223> OTHER INFORMATION: The amino acid residue at positions 1 or 2 can be
258       Leu, Ile, Val, Met, Phe, Tyr, or Trp.
260 <221> NAME/KEY: VARIANT
261 <222> LOCATION: 3,4,8-10,12,13
262 <223> OTHER INFORMATION: The amino acid residue at positions 3, 4, 8-10, 12
263       and 13 can be any amino acid.
265 <221> NAME/KEY: VARIANT
266 <222> LOCATION: 7
267 <223> OTHER INFORMATION: The amino acid residue at position 7 can be Asn or
268       His.
270 <221> NAME/KEY: VARIANT
271 <222> LOCATION: 11
272 <223> OTHER INFORMATION: The amino acid residue at position 11 can be Ser,
273       Asn, or Asp.
275 <221> NAME/KEY: VARIANT
276 <222> LOCATION: 14
277 <223> OTHER INFORMATION: The amino acid residue at position 14 can be Ser
278       or Gly.
280 <400> SEQUENCE: 8
281 Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
282  1              5                  10
285 <210> SEQ ID NO: 9
286 <211> LENGTH: 8
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: consensus
293 <221> NAME/KEY: VARIANT
294 <222> LOCATION: 1
295 <223> OTHER INFORMATION: The amino acid residue at position 1 can be Gly or
296       Ser.
298 <221> NAME/KEY: VARIANT
299 <222> LOCATION: 2,5
300 <223> OTHER INFORMATION: The amino acid residue at positions 2 and 5 can be
301       any amino acid.
303 <221> NAME/KEY: VARIANT
304 <222> LOCATION: 6
305 <223> OTHER INFORMATION: The amino acid residue at position 6 can be Pro or
306       Ser.
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/046,643**

DATE: 02/06/2002
TIME: 08:05:06

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\02062002\J046643.raw**

```
L:12  M:270 C: Current Application Number differs, Replaced Current Application No
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```

OIPE

RAW SEQUENCE LISTING   DATE: 01/28/2002
PATENT APPLICATION: US/10/046,643   TIME: 13:48:30

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF3\01282002\J046643.raw**

Does No Comply
Corrected Diskette Name

```
     4 <110> APPLICANT: Meyers, Rachel E.
     5        Millennium Pharmaceuticals Inc
     7 <120> TITLE OF INVENTION: 33449, A Human Protease Family Member
     8        and Uses Therefor
    10 <130> FILE REFERENCE: MPI2001-016P1RCP1(M)
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/046,643
C--> 12 <141> CURRENT FILING DATE: 2002-01-14
    12 <150> PRIOR APPLICATION NUMBER: 60/262,513
    13 <151> PRIOR FILING DATE: 2001-01-18
    15 <160> NUMBER OF SEQ ID NOS: 10
    17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
   323 <210> SEQ ID NO: 10
   324 <211> LENGTH: 13
   325 <212> TYPE: PRT
   326 <213> ORGANISM: Artificial Sequence
   328 <220> FEATURE:
   329 <223> OTHER INFORMATION: consensus
   331 <221> NAME/KEY: VARIANT
   332 <222> LOCATION: 3,4
   333 <223> OTHER INFORMATION: The amino acid residue at positions 3 or 4 can be
   334        Leu, Ile, Val, Met, Ser, Thr, or Ala.
   336 <221> NAME/KEY: VARIANT
   337 <222> LOCATION: 5
   338 <223> OTHER INFORMATION: The amino acid residue at position 5 can be Gly or
   339        Ala.
   341 <221> NAME/KEY: VARIANT
   342 <222> LOCATION: 6,10,12
   343 <223> OTHER INFORMATION: The amino acid residue at positions 6, 10, and 12
   344        can be any amino acid.
   346 <221> NAME/KEY: VARIANT
   347 <222> LOCATION: 7
   348 <223> OTHER INFORMATION: The amino acid residue at position 7 can be Pro or
   349        Gly.
   351 <221> NAME/KEY: VARIANT
   352 <222> LOCATION: 9
   353 <223> OTHER INFORMATION: The amino acid residue at position 9 can be Asp or
   354        Glu.
   356 <221> NAME/KEY: VARIANT
   357 <222> LOCATION: (11)
```

RAW SEQUENCE LISTING   DATE: 01/28/2002
PATENT APPLICATION: US/10/046,643   TIME: 13:48:30

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\01282002\J046643.raw

```
358 <223> OTHER INFORMATION: The amino acid residue at position 11 can be Leu,
359       Ile, Val, or Met.
361 <221> NAME/KEY: VARIANT
362 <222> LOCATION: (13)
363 <223> OTHER INFORMATION: The amino acid residue at position 13 can be Leu,
364       Ile, Val, Met, Phe, or Tyr.
366 <400> SEQUENCE: 10
```

W--> 367 Lys Arg Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa

```
368 1                   5                   10
```

E--> 370 (- 7 -)

VERIFICATION SUMMARY   DATE: 01/28/2002
PATENT APPLICATION: **US/10/046,643**   TIME: 13:48:31

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF3\01282002\J046643.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:370 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10